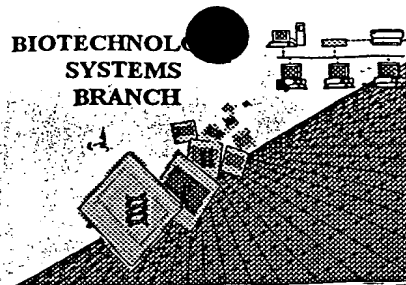


**RAW SEQUENCE LISTING
ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



7

BC

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/674,337

Source: PCT/09

Date Processed by STIC: 10/26/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/674,337

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

Please
Consult
Sequence Rules
 Does Not Comply
 Corrected Diskette Needed

see pp 1-15

4 <110> APPLICANT: Japan Science And Technology Corporation
 6 <120> TITLE OF INVENTION: Nicotianamine synthase, genes coding nicotianamine synthase
 8 <130> FILE REFERENCE: PA906235
 10 <140> CURRENT APPLICATION NUMBER: US/09/674,337
 10 <141> CURRENT FILING DATE: 2001-08-22
 10 <160> NUMBER OF SEQ ID NOS: 22

OK

ERRORED SEQUENCES

12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 328
 14 <212> TYPE: PRT
 15 <213> ORGANISM: Hordeum vulgare L.
 16 <400> SEQUENCE: 1

OK

18 Met Asp Ala Gln Asn Lys Glu Val Ala Ala Leu Ile Glu Lys Ile
 19 Ala Gly Ile Gln Ala Ala Ile Ala Glu Leu Pro Ser Leu Ser Pro
 20 Ser Pro Glu Val Asp Arg Leu Phe Thr Asp Leu Val Thr Ala Cys
 21 Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Ser Pro Glu His
 22 Gln Arg Met Arg Glu Ala Leu Ile Arg Leu Cys Ser Ala Ala Glu
 23 Gly Lys Leu Glu Ala His Tyr Ala Asp Leu Leu Ala Thr Phe Asp
 24 Asn Pro Leu Asp His Leu Gly Leu Phe Pro Tyr Tyr Ser Asn Tyr
 25 Val Asn Leu Ser Arg Leu Glu Tyr Glu Leu Leu Ala Arg His Val
 26 Pro Gly Ile Ala Pro Ala Arg Val Ala Phe Val Gly Ser Gly Pro
 27 Leu Pro Phe Ser Ser Leu Val Leu Ala Ala His His Leu Pro Glu
 28 Thr Gln Phe Asp Asn Tyr Asp Leu Cys Gly Ala Ala Asn Glu Arg
 29 Ala Arg Lys Leu Phe Gly Ala Thr Ala Asp Gly Val Gly Ala Arg
 30 Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Gln Glu Leu
 31 Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala
 32 Ala Glu Glu Lys Ala Lys Val Ile Ala His Leu Gly Ala His Met
 33 Val Glu Gly Ala Ser Leu Val Val Arg Ser Ala Arg Pro Arg Gly
 34 Phe Leu Tyr Pro Ile Val Asp Pro Glu Asp Ile Arg Arg Gly Gly
 35 Phe Glu Val Leu Ala Val His His Pro Glu Gly Glu Val Ile Asn
 36 Ser Val Ile Val Ala Arg Lys Ala Val Glu Ala Gln Leu Ser Gly
 37 Pro Gln Asn Gly Asp Ala His Ala Arg Gly Ala Val Pro Leu Val
 38 Ser Pro Pro Cys Asn Phe Ser Thr Lys Met Glu Ala Ser Ala Leu
 E--> 39 Glu Lys Ser Glu Glu Leu Thr Ala Lys Glu Leu Ala Phe

Per: Sequence Rules, number the
amino acids under every 5

amino acids.
DO NOT use
TAB codes between
NOS.

delete

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328

invalid
numbering

42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 1295
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Hordeum vulgare L.

W--> 46 <400> SEQUENCE: 2

E--> 47 10 20 30 40 50 60
 E--> 48 gcgttcagag gcttcagag ttcttcgggt caccaagaag catttgatca taacatggat 60
 E--> 50 70 80 90 100 110 120
 E--> 51 gccagaaca aggaggtcgc tgctctgatc gagaagatcg ccggtatcca ggcgccatc 120
 E--> 53 130 140 150 160 170 180

invalid numbering
delete

Per Sequence Rules,
insert cumulative
base total at right
margin
delete of
delete each
line

IMPORTANT: all bases MUST be in lower-case

letters when using new Sequence Rules format
 10/26/01

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

```

E--> 54 gccgagctgc cgtegetgag cccgtccccc gaggtcgaca ggctcttcac cgacctcgtc
E--> 56   190   200   210   220   230   240
E--> 57 acggcctgcg tcccgcgcag ccccgctcac gtgacgaagc tcagcccgga gcaccagagg
E--> 59   250   260   270   280   290   300
E--> 60 atgcgggagg ctctcatccg cttgtgctcc gccgcgcagg ggaagctcga ggcgcactac
E--> 62   310   320   330   340   350   360
E--> 63 gccgacctgc tcgccacctt cgacaacccg ctcgaccacc tcggcctctt cccgtactac
E--> 65   370   380   390   400   410   420
E--> 66 agcaactacg tcaacctcag caggtctggag tacgagctcc tggcgcgcca cgtgccgggc
E--> 68   430   440   450   460   470   480
E--> 69 atcgcgccgg cgcgcgtcgc cttcgtcggc tccggcccgc tgcggttcag ctcgctcgtc
E--> 71   490   500   510   520   530   540
E--> 72 ctcgccgcgc accacctgcc cgagaccagc ttcgacaact acgacctgtg cggcgcggcc
E--> 74   550   560   570   580   590   600
E--> 75 aacgagcgcg ccaggaagct gttcggcgcg acggcggacg gcgtcggcgc gcgtatgtcg
E--> 77   610   620   630   640   650   660
E--> 78 ttccacacgg cggacgtcgc cgacctcacc caggagctcg gcgcctacga cgtggtcttc
E--> 80   670   680   690   700   710   720
E--> 81 ctgcgccgcgc tcgtcggcat ggcagccgag gagaaggcca aggtgattgc ccacctgggc
E--> 83   730   740   750   760   770   780
E--> 84 gcgcacatgg tggagggggc gtccttggtc gtgcggagcg cagggccccg cggctttctt
E--> 86   790   800   810   820   830   840
E--> 87 taccctattg tcgaccgga ggacatcagg cggggtgggt tcgaggtgct ggccgtgcac
E--> 89   850   860   870   880   890   900
E--> 90 cacccggaag gtgaggtgat caactctgtc atcgtcgccc gtaaggccgt cgaagcgcag
E--> 92   910   920   930   940   950   960
E--> 93 ctcaagtggc cgcagaacgg agacgcgcac gcacggggcg cgggtgccgtt ggtcagcccc
E--> 95   970   980   990   1000   1010   1020
E--> 96 ccatgcaact tctccaccaa gatggaggcg agcgcgcttg agaagagcga ggagctgacc
E--> 98  1030   1040   1050   1060   1070   1080
E--> 99 gccaaagagc tggccttttg attgaagagt gcgcgtggtc attctgtcgc ctgcgatcgt
E--> 101  1090   1100   1110   1120   1130   1140
E--> 102 ggtaactttc ctactcgtgt gtgttttgat gtttgtgcct gtaagagtta tgcttccggc
E--> 104  1150   1160   1170   1180   1190   1200
E--> 105 cttgtgctgt taatttacac gcgttacatg tagtacttgt atttatacct ggaataacgg
E--> 107  1210   1220   1230   1240   1250   1260
E--> 108 tatgtaacat aaatattagt gggatttgaa gtgtaatgct aaataataag aaaacttgat
E--> 110  1270   1280   1290   1300
E--> 111 gcgacatttc aaaaaaaaaa aaaaaaaaaa aaaaa

```

*Please
insert
cumulative
base totals
at right
margin of
each line*

```

114 <210> SEQ ID NO: 3
115 <211> LENGTH: 335
116 <212> TYPE: PRT
117 <213> ORGANISM: Hordeum vulgare L.
118 <400> SEQUENCE: 3

```

same error as Sequence 1

```

120 Met Ala Ala Gln Asn Asn Gln Glu Val Asp Ala Leu Val Glu Lys
121 Ile Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser
122 Pro Ser Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr Ala
123 Cys Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu
124 Ala Gln Glu Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala

```

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

125 Glu Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe
 126 Asp Lys Pro Leu Asp His Leu Gly Met Phe Pro Tyr Tyr Asn Asn
 127 Tyr Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg Tyr
 128 Val Pro Gly Gly Tyr Arg Pro Ala Arg Val Ala Phe Ile Gly Ser
 129 Gly Pro Leu Pro Phe Ser Ser Phe Val Leu Ala Ala Arg His Leu
 130 Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu Cys Gly Ala Ala Asn
 131 Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Arg Asp Val Gly Ala
 132 Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Ala Gly Glu
 133 Leu Ala Lys Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met
 134 Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala His
 135 Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala His Gly Ala
 136 Arg Gly Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg
 137 Gly Gly Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Val
 138 Val Asn Ser Val Ile Ile Ala Gln Lys Ser Lys Asp Val His Ala
 139 Asp Gly Leu Gly Ser Gly Arg Gly Ala Gly Gly Gln Tyr Ala Arg
 140 Gly Thr Val Pro Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met
 141 Val Ala Asp Val Thr Gln Asn His Lys Arg Asp Glu Phe Ala Asn
 E--> 142 Ala Glu Val Ala Phe
 145 <210> SEQ ID NO: 4
 146 <211> LENGTH: 1342
 147 <212> TYPE: DNA
 148 <213> ORGANISM: Hordeum vulgare L.
 W--> 149 <400> SEQUENCE: 4
 E--> 151 10 20 30 40 50 60
 E--> 152 ctctgtgccc tgtcctgagg taccaagaac accagtgaac tggctgcccga gaacaaccag
 E--> 154 70 80 90 100 110 120
 E--> 155 gaggtggatg ccctgggtgga gaagatcacc gggctccatg ccgcaatcgc caagctgccc
 E--> 157 130 140 150 160 170 180
 E--> 158 tcgctcagcc catccccgga cgtcgacgcg ctcttcacgg agctgggtcac ggcgtgcgtt
 E--> 160 190 200 210 220 230 240
 E--> 161 ccaccgagtc cagtggacgt gaccaagctc gggccggagg cgcaggagat gcgggagggc
 E--> 163 250 260 270 280 290 300
 E--> 164 ctcatccgcc tatgctccga ggccgagggg aagctggagg cgcactactc cgacatgctc
 E--> 166 310 320 330 340 350 360
 E--> 167 gccgccttcg acaagccgct ggatcacctc ggcatgttcc cctactacaa caactacatc
 E--> 169 370 380 390 400 410 420
 E--> 170 aacctcagca agctcgagta cgagctcctg gcccgctacg tgcttgccgg ctatcgccc
 E--> 172 430 440 450 460 470 480
 E--> 173 gcgcgcgctg cgttcacgg ctccggcccg ctgccgttca gctcctttgt cctggccg
 E--> 175 490 500 510 520 530 540
 E--> 176 cgccacctgc ccgacaccat gttcgacaac tatgacctgt gcggtgcggc caacgatcgc
 E--> 178 550 560 570 580 590 600
 E--> 179 gccagcaagc tcttcgcgc ggatcgcgac gtgggtgccc gcatgtcggt ccacacggcc
 E--> 181 610 620 630 640 650 660
 E--> 182 gacgtcgcg acctcgccgg cgagctcgcc aagtacgacg ttgtcttctt ggccgcactc
 E--> 184 670 680 690 700 710 720
 E--> 185 gtcggcatgg ccgcccagga caaggcgaag gtgatcgcg acctcgccgc acacatggca
 E--> 187 730 740 750 760 770 780
 E--> 188 gacggggcgg ccctcgctgt ggcgagcgca cacggagcgc gcgggttctt gtacccgatc

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invalid
 numbering
 follow directions
 on p. 1

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

```

E--> 190      790      800      810      820      830      840
E--> 191 gtcgaccccc aggacatcgg ccgaggcggg ttcgaggtgc tggccgtgtg ccatcccgcac
E--> 193      850      860      870      880      890      900
E--> 194 gacgacgtgg tgaactccgt catcatcgca cagaagtcca aggacgtgca tgccgatgga
E--> 196      910      920      930      940      950      960
E--> 197 cttggcagcg ggcgtggtgc cgggtggacag tacgcgcggg gcacggtgcc tgttgtcagc
E--> 199      970      980      990      1000      1010      1020
E--> 200 cccccgtgca ggttcggcga gatggtggcg gacgtgaccc agaaccacaa gagagacgag
E--> 202      1030      1040      1050      1060      1070      1080
E--> 203 tttgccaacg ccgaagtggc cttttgatcg ttcgctgcga ggggtgtgcat ccatgatcca
E--> 205      1090      1100      1110      1120      1130      1140
E--> 206 tccatacctc gttctgtgat tgcatacgc ttgcaatcgt atgcatttca agtcacgtgt
E--> 208      1150      1160      1170      1180      1190      1200
E--> 209 tgctttctatc caataatgta cgtgtggtgt ttacacgcga atgtcttgta gacctttgta
E--> 211      1210      1220      1230      1240      1250      1260
E--> 212 tgtgtacaag tgaattttta ttcacaagta catataatgg tcaccattga aaagatgttt
E--> 214      1270      1280      1290      1300      1310      1320
E--> 215 agtgtgtgtt ttccaatata tgtttgtgta aggttcatca tctaataaaa tatgtttgga
E--> 217      1330      1340      1350

```

E--> 218 acccaaaaaa aaaaaaaaaa aa

221 <210> SEQ ID NO: 5

222 <211> LENGTH: 335

223 <212> TYPE: PRT

224 <213> ORGANISM: Hordeum vulgare L.

W--> 225 <400> SEQUENCE: 5

```

227 Met Ala Ala Gln Asn Asn Asn Lys Asp Val Ala Ala Leu Val Glu
228 Lys Ile Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu
229 Ser Pro Ser Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr
230 Ala Cys Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro
231 Glu Ala Gln Glu Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu
232 Ala Glu Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala
233 Phe Asp Asn Pro Leu Asp His Leu Gly Ile Phe Pro Tyr Tyr Ser
234 Asn Tyr Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg
235 Tyr Val Arg Arg His Arg Pro Ala Arg Val Ala Phe Ile Gly Ser
236 Gly Pro Leu Pro Phe Ser Ser Phe Val Leu Ala Ala Arg His Leu
237 Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu Cys Gly Ala Ala Asn
238 Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Thr Asp Val Gly Ala
239 Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Ala Ser Glu
240 Leu Ala Lys Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met
241 Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala His
242 Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala His Gly Ala
243 Arg Gly Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg
244 Gly Gly Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val
245 Val Asn Ser Val Ile Ile Ala Gln Lys Ser Lys Glu Val His Ala
246 Asp Gly Leu Gly Ser Ala Arg Gly Ala Gly Arg Gln Tyr Ala Arg
247 Gly Thr Val Pro Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met
248 Val Ala Asp Val Thr Gln Asn His Lys Arg Asp Glu Phe Ala Asn
E--> 249 Ala Glu Val Ala Phe

```

252 <210> SEQ ID NO: 6

*same error**same error as p. 1*

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

253 <211> LENGTH: 1314

254 <212> TYPE: DNA

255 <213> ORGANISM: Hordeum vulgare L.

W--> 256 <400> SEQUENCE: 6

```

E--> 257      10      20      30      40      50      60
E--> 258 ctacttcact cacactagtg cccagaaaaga aggctgcaat ggctgcccag aacaacaaca
E--> 260      70      80      90     100     110     120
E--> 261 aggatgtcgc tgccctgggtg gagaagatca cggggctcca cgccgccatc gccaaactgc
E--> 263     130     140     150     160     170     180
E--> 264 cgtcgctcag cccatccccg gacgtcgacg cgctcttcac cgagctggtc acggcgtgcg
E--> 266     190     200     210     220     230     240
E--> 267 ttcccccgag ccccggtggac gtgaccaagc tcggccccga ggcgcaggag atgcggggagg
E--> 269     250     260     270     280     290     300
E--> 270 gcctcatecg cctctgctcc gagggcggagg ggaagctgga ggcgcactac tccgacatgc
E--> 272     310     320     330     340     350     360
E--> 273 tcgcccgcctt cgacaacccg ctggatcacc tcggcatctt cccctactac agcaactaca
E--> 275     370     380     390     400     410     420
E--> 276 tcaacctcag caagctggag tacgagctcc tggcacgcta cgctccggcg catcgcccg
E--> 278     430     440     450     460     470     480
E--> 279 cccgcgtcgc gttcatcggc tccggccccg tgccgttcag ctctttgtc ctggccgcgc
E--> 281     490     500     510     520     530     540
E--> 282 gccacctgcc cgacaccatg tttgacaact acgacctttg cggcgcgggc aacgatcgcg
E--> 284     550     560     570     580     590     600
E--> 285 ccagcaagct cttccgcgcg gacacggacg tgggtgcccc catgtcgttc cacacggccg
E--> 287     610     620     630     640     650     660
E--> 288 acgtcgcgga cctcgccagc gagctcgcca agtacgacgt cgtcttcttg gccgcgctcg
E--> 290     670     680     690     700     710     720
E--> 291 tcggcatggc cgccgaggac aaggccaagg tgatcgcgca cctcggcgca cacatggcag
E--> 293     730     740     750     760     770     780
E--> 294 acggggcggc cctcgctcgtg cgcagcgcac acggagcgcg cgggttcctg tacccgattg
E--> 296     790     800     810     820     830     840
E--> 297 tcgacccccg ggacatcggc cgcggcgggg tcgaggtgct ggccgtgtgc caccgccgac
E--> 299     850     860     870     880     890     900
E--> 300 acgacgtggt gaactccgtc atcatcgcac agaagtccaa ggaggtgcat gccgatggac
E--> 302     910     920     930     940     950     960
E--> 303 ttggcagcgc gcgtggtgcc ggctcgacagt acgcgcgcgg cacggtgccg gttgtcagcc
E--> 305     970     980     990    1000    1010    1020
E--> 306 ccccggtgcag gttcggtgag atggtggcgg atgtgaccca gaaccacaag agagacgagt
E--> 308    1030    1040    1050    1060    1070    1080
E--> 309 ttgccaacgc cgaagtggcc ttttgatcga tcgtcgccaa gggacaataa atgaacgtgg
E--> 311    1090    1100    1110    1120    1130    1140
E--> 312 atgtggtagg gtaatttgcc tacctcgctg cttgatcgct tgcaatatgt gcacattttc
E--> 314    1150    1160    1170    1180    1190    1200
E--> 315 ctactaccgc tgcttatgca tttcaagcca tgtgatgttg gtatccaata aagtatgtgt
E--> 317    1210    1220    1230    1240    1250    1260
E--> 318 aggggtttaca cgcaaagtgc tttacacctt gtacgtgtaa gtgttgacaa cgatgaattt
E--> 320    1270    1280    1290    1300    1310    1320
E--> 321 cagttcacaa ttaataaata gtataatgga ttcaaaaaaa aaaaaaaaaa aaaa
324 <210> SEQ ID NO: 7

```

*inserted
numbers*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

325 <211> LENGTH: 329

326 <212> TYPE: PRT

327 <213> ORGANISM: Hordeum vulgare L.

W--> 328 <400> SEQUENCE: 7

330	Met	Asp	Gly	Gln	Ser	Glu	Glu	Val	Asp	Ala	Leu	Val	Gln	Lys	Ile	15
331	Thr	Gly	Leu	His	Ala	Ala	Ile	Ala	Lys	Leu	Pro	Ser	Leu	Ser	Pro	30
332	Ser	Pro	Asp	Val	Asp	Ala	Leu	Phe	Thr	Asp	Leu	Val	Thr	Ala	Cys	45
333	Val	Pro	Pro	Ser	Pro	Val	Asp	Val	Thr	Lys	Leu	Ala	Pro	Glu	Ala	60
334	Gln	Ala	Met	Arg	Glu	Gly	Leu	Ile	Arg	Leu	Cys	Ser	Glu	Ala	Glu	75
335	Gly	Lys	Leu	Glu	Ala	His	Tyr	Ser	Asp	Met	Leu	Ala	Ala	Phe	Asp	90
336	Asn	Pro	Leu	Asp	His	Leu	Gly	Val	Phe	Pro	Tyr	Tyr	Ser	Asn	Tyr	105
337	Ile	Asn	Leu	Ser	Lys	Leu	Glu	Tyr	Glu	Leu	Leu	Ala	Arg	Tyr	Val	120
338	Pro	Gly	Arg	His	Arg	Pro	Ala	Arg	Val	Ala	Phe	Ile	Gly	Ser	Gly	135
339	Pro	Leu	Pro	Phe	Ser	Ser	Tyr	Val	Leu	Ala	Ala	Arg	His	Leu	Pro	150
340	Asp	Thr	Val	Phe	Asp	Asn	Tyr	Asp	Leu	Cys	Gly	Ala	Ala	Asn	Asp	165
341	Arg	Ala	Thr	Arg	Leu	Phe	Arg	Ala	Asp	Lys	Asp	Val	Gly	Ala	Arg	180
342	Met	Ser	Phe	His	Thr	Ala	Asp	Val	Ala	Asp	Leu	Thr	Asp	Glu	Leu	195
343	Ala	Thr	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	Met	Ala	210
344	Ala	Glu	Asp	Lys	Ala	Lys	Val	Ile	Ala	His	Leu	Gly	Ala	His	Met	225
345	Ala	Asp	Gly	Ala	Ala	Leu	Val	Ala	Arg	His	Gly	Ala	Arg	Gly	Phe	240
346	Leu	Tyr	Pro	Ile	Val	Asp	Pro	Gln	Asp	Ile	Gly	Arg	Gly	Gly	Phe	255
347	Glu	Val	Leu	Ala	Val	Cys	His	Pro	Asp	Asp	Asp	Val	Val	Asn	Ser	270
348	Val	Ile	Ile	Ala	Gln	Lys	Ser	Asn	Asp	Val	His	Glu	Tyr	Gly	Leu	285
349	Gly	Ser	Gly	Arg	Gly	Gly	Arg	Tyr	Ala	Arg	Gly	Thr	Val	Val	Pro	300
350	Val	Val	Ser	Pro	Pro	Cys	Arg	Phe	Gly	Glu	Met	Val	Ala	Asp	Val	315
E--> 351	Thr	Gln	Lys	Arg	Glu	Glu	Phe	Ala	Asn	Ala	Glu	Val	Ala	Phe		329

involved
nos

353 <210> SEQ ID NO: 8

354 <211> LENGTH: 1249

355 <212> TYPE: DNA

356 <213> ORGANISM: Hordeum vulgare L.

W--> 357 <400> SEQUENCE: 8

E--> 359	10	20	30	40	50	60
E--> 360	ccactaccga	ctaccgtagt	accgtgcctc	agagctcatc	actgggtcagg	taccaagaag
E--> 362	70	80	90	100	110	120
E--> 363	acataaaaat	ggacggccag	agcgaggagg	tcgacgccct	tgtccagaag	atcaccggcc
E--> 365	130	140	150	160	170	180
E--> 366	tccacgccgc	catcgccaag	ctgccctcgc	tcagcccgtc	cccggacgtc	gacgcgctct
E--> 368	190	200	210	220	230	240
E--> 369	tcaccgacct	ggtcaccgcg	tgcgtgcccc	cgagccccgt	ggacgtgacc	aagctcgccc
E--> 371	250	260	270	280	290	300
E--> 372	cggaggcgca	ggcgatgcgg	gagggcctca	tccgcctctg	ctccgaggcc	gagggcaagc
E--> 374	310	320	330	340	350	360
E--> 375	tggaggcgca	ctactccgac	atgctcgccg	ccttcgacaa	cccgtcgcac	cacctcgccg
E--> 377	370	380	390	400	410	420
E--> 378	tcttccccta	ctacagcaac	tacatcaacc	tcagcaagct	tgagtacgag	ctcctcgccg
E--> 380	430	440	450	460	470	480
E--> 381	gctacgtgcc	cggcaggcat	cgccccggcc	gcgtcgccct	catcggtccc	ggccccgtgc
E--> 383	490	500	510	520	530	540
E--> 384	cgttcagctc	ctacgtcctc	gccgcgcgcc	acctgcccga	caccgtgttc	gacaactacg

involved

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set : N:\CRF3\10262001\I674337.raw

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E--> 386      550      560      570      580      590      600
E--> 387 acctgtgcgg cgcggccaac gaccgcgcga ccaggctgtt ccgcgcggac aaggacgtcg
E--> 389      610      620      630      640      650      660
E--> 390 gcgcccgcac gtcgttcac accgccgacg tcgcggacct caccgacgag ctcgctacgt
E--> 392      670      680      690      700      710      720
E--> 393 acgacgtcgt cttcctggcc gcgctcgtgg gcatggccgc cgaggacaag gccaaagtga
E--> 395      730      740      750      760      770      780
E--> 396 tcgcgcacct tggcgcgcac atggcggacg gggcggccct cgttgccggg caccggcgcg
E--> 398      790      800      810      820      830      840
E--> 399 gtgggttcct ctaccgatc gtcgatcccc aggacatcgg tcgaggcggg ttcgaggtgc
E--> 401      850      860      870      880      890      900
E--> 402 tcgccgtgtg tcaccccgac gacgacgtgg tgaactccgt catcatcgca caaaagagca
E--> 404      910      920      930      940      950      960
E--> 405 acgacgtgca cgagtatgga cttggcagcg ggcgtggtgg acggtacgcg cgaggcacgg
E--> 407      970      980      990      1000      1010      1020
E--> 408 tggtgccggt ggtcagccca ccctgcaggt tcggcgcgat ggtggcagac gtgaccaga
E--> 410      1030      1040      1050      1060      1070      1080
E--> 411 agagagagga gtttgccaac gcggaagtgg ccttctgatt gctgctgaat cgcttgtgat
E--> 413      1090      1100      1110      1120      1130      1140
E--> 414 cgtacgtggt aatttttcta ctactctcc tcctaccacc acctatcacc tatgtatgca
E--> 416      1150      1160      1170      1180      1190      1200
E--> 417 tttcaagtcg tgtgttgttt gtatccaata atgtaagtga gatgtttaca cgcgcaaaaa
E--> 419      1210      1220      1230      1240      1250
E--> 420 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

```

423 <210> SEQ ID NO: 9

424 <211> LENGTH: 282

425 <212> TYPE: PRT

426 <213> ORGANISM: Hordeum vulgare L.

W--> 427 <400> SEQUENCE: 9

```

429 Met Glu Ala Glu Asn Gly Glu Val Ala Ala Leu Val Glu Lys Ile      15
430 Thr Gly Leu His Ala Ala Ile Ser Lys Leu Pro Ala Leu Ser Pro      30
431 Ser Pro Gln Val Asp Ala Leu Phe Thr Glu Leu Val Ala Ala Cys      45
432 Val Pro Ser Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu Ala      60
433 Gln Glu Met Arg Gln Asp Leu Ile Arg Leu Cys Ser Ala Ala Glu      75
434 Gly Leu Leu Glu Ala His Tyr Ser Asp Met Leu Thr Ala Leu Asp      90
435 Ser Pro Leu Asp His Leu Gly Arg Phe Pro Tyr Phe Asp Asn Tyr     105
436 Val Asn Leu Ser Lys Leu Glu His Asp Leu Leu Ala Gly His Val     120
437 Ala Ala Pro Ala Arg Val Ala Phe Ile Gly Ser Gly Pro Leu Pro     135
438 Phe Ser Ser Leu Phe Leu Ala Thr Tyr His Leu Pro Asp Thr Arg     150
439 Phe Asp Asn Tyr Asp Arg Cys Ser Val Ala Asn Gly Arg Ala Met     165
440 Lys Leu Val Gly Ala Ala Asp Glu Gly Val Arg Ser Arg Met Ala     180
441 Phe His Thr Ala Glu Val Thr Asp Leu Thr Ala Glu Leu Gly Ala     195
442 Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Thr Ser Lys     210
443 Glu Lys Ala Asp Ala Ile Ala His Leu Gly Lys His Met Ala Asp     225
444 Gly Ala Val Leu Val Arg Glu Ala Leu His Gly Ala Arg Ala Phe     240
445 Leu Tyr Pro Val Val Glu Leu Asp Asp Val Gly Arg Gly Gly Phe     255
446 Gln Val Leu Ala Val His His Pro Ala Gly Asp Glu Val Phe Asn     270
E--> 447 Ser Phe Ile Val Ala Arg Lys Val Lys Met Ser Ala      282
449 <210> SEQ ID NO: 10

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

450 <211> LENGTH: 1044

451 <212> TYPE: DNA

452 <213> ORGANISM: Hordeum vulgare L.

W--> 453 <400> SEQUENCE: 10

```

E--> 455      10      20      30      40      50      60
E--> 456 gtgacatgga ggccgaaaac ggcgaggtgg ctgctctggt cgagaagatc accggtctcc
E--> 458      70      80      90     100     110     120
E--> 459 acgccgccat ctccaagctc ccggcactaa gcccgtctcc tcaagtcgac gcgctcttca
E--> 461     130     140     150     160     170     180
E--> 462 ccgagctggt tgcggcgtgc gtcccatcaa gcccgggtgga cgtgaccaag ctcggtcccg
E--> 464     190     200     210     220     230     240
E--> 465 aggcgcagga gatgcggcag gacctcatcc gtctctgctc ggccgcccag gggctgctcg
E--> 467     250     260     270     280     290     300
E--> 468 aggcgcacta ctccgacatg ctccaccgct tggacagccc gctcgaccac ctcggtccgct
E--> 470     310     320     330     340     350     360
E--> 471 tcccttactt cgacaactac gtcaacctca gcaagctcga gcacgatctt ctggcaggctc
E--> 473     370     380     390     400     410     420
E--> 474 acgtggcggc cccggcccg cgtggcgttca tcgggtcggg gccactgccg ttcagctcgc
E--> 476     430     440     450     460     470     480
E--> 477 tcttccttgc gacgtaccac ctgccggaca cccggttcga caactacgac cgggtgcagcg
E--> 479     490     500     510     520     530     540
E--> 480 tggcgaatgg ccgggcgatg aagctggctg gcgcggcgga cgagggcgctg cgatcacgca
E--> 482     550     560     570     580     590     600
E--> 483 tggcggtcca caccggcgaa gtcacggacc tcacggctga gctcggcgct tacgacgtgg
E--> 485     610     620     630     640     650     660
E--> 486 tcttcctggc cgcgctcgtg ggaatgacgt ccaaggagaa ggccgacgcc atagcgcact
E--> 488     670     680     690     700     710     720
E--> 489 tggggaagca catggcagat ggggcggtgc tcgtgcgcga agcgctgcac ggggcgcgag
E--> 491     730     740     750     760     770     780
E--> 492 cgttcctgta tctgtcgtg gagctggacg atgtcgggcg tgggtgggttc caagtgtggtg
E--> 494     790     800     810     820     830     840
E--> 495 ccgtgcacca ccctgcaggc gatgaggtgt tcaactcatt catagtgtgcc cggaagggtga
E--> 497     850     860     870     880     890     900
E--> 498 aaatgagtgc ttaaattaag aaaagggtga gcctgtctgc ttgtgcaa at ggtgtctcac
E--> 500     910     920     930     940     950     960
E--> 501 attgataata accagatgat accctgcaca ttgatggggg tactgcagta tgtttcaatg
E--> 503     970     980     990    1000    1010    1020
E--> 504 aggtctggtt gtatcaaata tgagtatttg gcttaataat atcagcgaat atgtttcgat
E--> 506    1030    1040    1050
E--> 507 taaaaaaaaa aaaaaaaaaa aaaa

```

invalid

509 <210> SEQ ID NO: 11

510 <211> LENGTH: 328

511 <212> TYPE: PRT

512 <213> ORGANISM: Hordeum vulgare L.

W--> 513 <400> SEQUENCE: 11

```

515 Met Asp Ala Gln Asn Lys Glu Val Asp Ala Leu Val Gln Lys Ile
516 Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro
517 Ser Pro Asp Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys
518 Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Ser Glu Ala

```

15
30
45
60*invalid*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

519 Gln Glu Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu 75
 520 Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp 90
 521 Asn Pro Leu Asp His Leu Gly Met Phe Pro Tyr Tyr Ser Asn Tyr 105
 522 Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg Tyr Val 120
 523 Pro Gly Gly Ile Ala Arg Pro Ala Val Ala Phe Ile Gly Ser Gly 135
 524 Pro Leu Pro Phe Ser Ser Tyr Val Leu Ala Ala Arg His Leu Pro 150
 525 Asp Ala Met Phe Asp Asn Tyr Asp Leu Cys Ser Ala Ala Asn Asp 165
 526 Arg Ala Ser Lys Leu Phe Arg Ala Asp Lys Asp Val Gly Ala Arg 180
 527 Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Arg Glu Leu 195
 528 Ala Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala 210
 529 Ala Glu Asp Lys Ala Lys Val Ile Pro His Leu Gly Ala His Met 225
 530 Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala Gln Ala Arg Gly 240
 531 Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly Gly 255
 532 Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn 270
 533 Ser Val Ile Ile Ala His Lys Ser Lys Asp Val His Ala Asn Glu 285
 534 Arg Pro Asn Gly Arg Gly Gly Gln Tyr Arg Gly Ala Val Pro Val 300
 535 Val Ser Pro Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val Thr 315
 E--> 536 His Lys Arg Glu Glu Phe Thr Asn Ala Glu Val Ala Phe 328
 539 <210> SEQ ID NO: 12
 540 <211> LENGTH: 1352
 541 <212> TYPE: DNA
 542 <213> ORGANISM: Hordeum vulgare L.
 W--> 543 <400> SEQUENCE: 12
 E--> 545 10 20 30 40 50 60
 E--> 546 ctccacttcg ctccctgtgcc tcaggtagcc acaacataca gtattaaaat ggatgcccaag
 E--> 548 70 80 90 100 110 120
 E--> 549 aacaaggagg ttgatgccct ggtccagaag atcaccggcc tccacgccgc catcgccaag
 E--> 551 130 140 150 160 170 180
 E--> 552 ctgccgtccc tcagcccatc acccgacgtc gacgcgtctt tcaccgacct ggtcaccgcg
 E--> 554 190 200 210 220 230 240
 E--> 555 tgcggtcccc cgagccccgt ggacgtgacc aagctcgggt cggaggcgca ggagatgcgg
 E--> 557 250 260 270 280 290 300
 E--> 558 gagggcctca tccgcctctg ctccgaggcc gaggggaagc tggaggcgca ctactccgac
 E--> 560 310 320 330 340 350 360
 E--> 561 atgctggccg ccttcgacaa cccgctcgac cacctcggca tgttccccta ctacagcaac
 E--> 563 370 380 390 400 410 420
 E--> 564 tacatcaacc tcagcaagct ggagtagcag ctccctggcg gctacgtgcc gggcgccatc
 E--> 566 430 440 450 460 470 480
 E--> 567 gcccggcccc ctgtcgcggt catcggtccc ggcccgtgc cgttcagctc ctacgtcttc
 E--> 569 490 500 510 520 530 540
 E--> 570 gccgctcgcc acctgcccga cgccatgttc gacaactacg acctgtgtag cgcgccaac
 E--> 572 550 560 570 580 590 600
 E--> 573 gaccgtgcga gcaagctgtt ccgcgcggac aaggacgtgg gcgcccgcgt gtctttccac
 E--> 575 610 620 630 640 650 660
 E--> 576 accgcccagc tagcggacct caccgcgag ctcgccgct acgacgtcgt cttcctggcc
 E--> 578 670 680 690 700 710 720
 E--> 579 gcgctcgtgg gcatggctgc cgaggacaag gccaaagtga ttccgcacct cggcgcgcac
 E--> 581 730 740 750 760 770 780
 E--> 582 atggcgagc gggcgccct cgtcgtgcgc agtgcgagc cacgtgggtt cctctaccgc

*invalid**invalid*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

```

E--> 584      790      800      810      820      830      840
E--> 585 atcgtcgatc cccaggacat cggtcgaggc gggtttgagg tgctggccgt gtgtcacccc
E--> 587      850      860      870      880      890      900
E--> 588 gacgatgacg tggatgaactc cgtcatcatc gcacacaagt ccaaggacgt gcatgccaat
E--> 590      910      920      930      940      950      960
E--> 591 gaacgtccca acggggcgtgg tggacagtac cggggcgcgcg taccgggtgg cagcccgcgg
E--> 593      970      980      990      1000      1010      1020
E--> 594 tgcaggttcg gtgagatggg ggcggacgtg acccacaaga gagaggagtt caccaacgcg
E--> 596      1030      1040      1050      1060      1070      1080
E--> 597 gaagtggcct tctgatcggt gcgagggaaat gaaaatgaag gtggacgtgt gtggtcagca
E--> 599      1090      1100      1110      1120      1130      1140
E--> 600 tccatacgtg gctgcctgct tcatcgcttg caatcgtagt actacctacc tatgcagttc
E--> 602      1150      1160      1170      1180      1190      1200
E--> 603 aagtcagtgt ttgtcaatgt aagtgtgatg tttacactag tctatgaaag gcagggcaga
E--> 605      1210      1220      1230      1240      1250      1260
E--> 606 cgagggtagt gtgccaagta acagtgtgtc attataggtg taagtgttga gaataagacc
E--> 608      1270      1280      1290      1300      1310      1320
E--> 609 atttttgttc acaaatagta tgatgtaatc ggtgtcatat tcgtattgag tacatttgc
E--> 611      1330      1340      1350      1360
E--> 612 aagttggttg ctaaaaaaaaa aaaaaaaaa aa

```

615 <210> SEQ ID NO: 13

616 <211> LENGTH: 329

617 <212> TYPE: PRT

618 <213> ORGANISM: Hordeum vulgare L.

W--> 619 <400> SEQUENCE: 13

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621 Met Asp Ala Gln Ser Lys Glu Val Asp Ala Leu Val Gln Lys Ile      15
622 Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro      30
623 Ser Pro Asp Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys      45
624 Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Ala Pro Glu Ala      60
625 Gln Ala Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu      75
626 Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp      90
627 Asn Pro Leu Asp His Leu Gly Val Phe Pro Tyr Tyr Ser Asn Tyr     105
628 Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg Tyr Val     120
629 Pro Gly Gly Ile Ala Pro Ala Arg Val Ala Phe Ile Gly Ser Gly     135
630 Pro Leu Pro Phe Ser Ser Tyr Val Leu Ala Ala Arg His Leu Pro     150
631 Asp Thr Val Phe Asp Asn Tyr Val Pro Val Arg Ala Ala Asn Asp     165
632 Arg Ala Thr Arg Leu Phe Arg Ala Asp Lys Asp Val Gly Ala Arg     180
633 Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Asp Glu Leu     195
634 Ala Thr Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala     210
635 Ala Glu Asp Lys Gly Gln Gly Asp Pro His Leu Gly Ala His Met     225
636 Ala Asp Gly Ala Ala Leu Val Arg Ser Ala His Gly Ala Arg Gly     240
637 Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly Gly     255
638 Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Val Val Asn         270
639 Ser Val Ile Ile Ala Gln Lys Ser Lys Asp Met Phe Ala Asn Gly     285
640 Pro Arg Asn Gly Cys Gly Gly Arg Tyr Ala Arg Gly Thr Val Pro     300
641 Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val     315
E--> 642 Thr Gln Lys Arg Glu Glu Phe Ala Lys Ala Glu Val Ala Phe     329
646 <210> SEQ ID NO: 14
647 <211> LENGTH: 1371

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

648 <212> TYPE: DNA

649 <213> ORGANISM: Hordeum vulgare L.

W--> 650 <400> SEQUENCE: 14

	10	20	30	40	50
E--> 652	ggagcgggac	gcgtggcgga	ggtgggcact	accgtagtac	cgtgcctcag
E--> 653	60	70	80	90	100
E--> 654	agctcatcac	tggtcaggta	ccaagaagac	ataaaaatgg	acgcccagag
E--> 655	110	120	130	140	150
E--> 656	caaggaggtc	gacgcccttg	tccagaagat	caccggcctc	cacgcccga
E--> 657	160	170	180	190	200
E--> 658	tcgccaagct	gccctcgctc	agcccgtccc	cggacgtcga	cgcgctcttc
E--> 659	210	220	230	240	250
E--> 660	accgacctgg	tcaccgcgtg	cgtgcccccg	agccccgtgg	acgtgaccaa
E--> 661	260	270	280	290	300
E--> 662	gctcgccccg	gaggcgcagg	cgatgcggga	gggcctcatc	cgcctctgct
E--> 663	310	320	330	340	350
E--> 664	ccgaggccga	gggcaagctg	gaggcgcact	actccgacat	gctcgccgcc
E--> 665	360	370	380	390	400
E--> 666	ttcgacaacc	cgctcgacca	cctcggcgtc	ttccccctact	acagcaacta
E--> 667	410	420	430	440	450
E--> 668	catcaacctc	agcaagctcg	agtacgagct	cctcgcgcgc	tacgtgcccg
E--> 669	460	470	480	490	500
E--> 670	gcggcatcgc	cccggccccg	gtcgccttca	tcggctccgg	cccgtctccg
E--> 671	510	520	530	540	550
E--> 672	ttcagctcct	acgtcctcgc	cgcgcgccac	ctgcccga	ccgtgttcga
E--> 673	560	570	580	590	600
E--> 674	caactacgta	cctgtgcgcg	cggccaacga	ccgcgcgacc	aggctgttcc
E--> 675	610	620	630	640	650
E--> 676	gcgcggacaa	ggacgtcggc	gcccgcattg	cgttccacac	cgccgacgtc
E--> 677	660	670	680	690	700
E--> 678	gcggacctca	ccgacgagct	cgctacgtac	gacgtcgtct	tcctggccgc
E--> 679	710	720	730	740	750
E--> 680	gctcgtgggc	atggccgccg	aggacaaggg	ccaaggtgat	ccgcaccttg
E--> 681	760	770	780	790	800
E--> 682	gcgcgcacat	ggcggacggg	gcggccctcg	tccgcagcgc	gcacggggcg
E--> 683	810	820	830	840	850
E--> 684	cgtgggttcc	tctacccgat	cgtegatccc	caagacattg	gtcgaggcgg
E--> 685	860	870	880	890	900
E--> 686	gttcgaggtg	ctcgcctgtg	gtcaccgccg	cgacgacgtg	gtgaactccg
E--> 687	910	920	930	940	950
E--> 688	tcatcatcgc	gcagaagtct	aaggacatgt	ttgccaatgg	acctcgcaac
E--> 689	960	970	980	990	1000
E--> 690	gggtgtggtg	gacgggtacg	gcgaggcacg	gtgccggtgg	tcagcccgcc
E--> 691	1010	1020	1030	1040	1050
E--> 692	ctgcagggtt	ggcgagatgg	tggcagacgt	gaccagaag	agagaggagt
E--> 693	1060	1070	1080	1090	1100
E--> 694	ttgccaaggg	ggaagtggcc	ttctgattgc	tgcgagggtc	ccatccgtat
E--> 695	1110	1120	1130	1140	1150
E--> 696	gccgctgcta	cctttcaata	tcttgcaatc	gtaggtggcg	attttcctac
E--> 697					

also, see
item 9 on
Erra Summary
Sheet

Invalid
nos.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001
TIME: 15:00:33

Input Set : A:\55107-sequence.txt
Output Set: N:\CRF3\10262001\I674337.raw

```

E--> 698      1160      1170      1180      1190      1200
E--> 699 tcttggttacg acctttcaaa tcatatgttg tttgtaccca ataatgtaag
E--> 700      1210      1220      1230      1240      1250
E--> 701 tgtggttgctt acacgcgcac gtcttggtaca ctcggtctct agaaggcagg
E--> 702      1260      1270      1280      1290      1300
E--> 703 gcagatcaag agactgtgca aaggaaaaga aatgtgtgtt gttgtaggtg
E--> 704      1310      1320      1330      1340      1350
E--> 705 tatgagttgg gagtaagatg attctagttc acaaaaaaaaaa aaaaaaaaaa
E--> 706      1360      1370      1380
E--> 707 aaaaaaaaaa aaaaaaaaaa a

```

711 <210> SEQ ID NO: 15
712 <211> LENGTH: 332
713 <212> TYPE: PRT
714 <213> ORGANISM: Oryza sativa L.

W--> 715 <400> SEQUENCE: 15

```

717 Met Glu Ala Gln Asn Gln Glu Val Ala Ala Leu Val Glu Lys Ile 15
718 Ala Gly Leu His Ala Ala Ile Ser Lys Leu Pro Ser Leu Ser Pro 30
719 Ser Ala Glu Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys 45
720 Val Pro Ala Ser Pro Val Asp Val Ala Lys Leu Gly Pro Glu Ala 60
721 Gln Ala Met Arg Glu Glu Leu Ile Arg Leu Cys Ser Ala Ala Glu 75
722 Gly His Leu Glu Ala His Tyr Ala Asp Met Leu Ala Ala Phe Asp 90
723 Asn Pro Leu Asp His Leu Ala Arg Phe Pro Tyr Tyr Gly Asn Tyr 105
724 Val Asn Leu Ser Lys Leu Glu Tyr Asp Leu Leu Val Arg Tyr Val 120
725 Pro Gly Ile Ala Pro Thr Arg Val Ala Phe Val Gly Ser Gly Pro 135
726 Leu Pro Phe Ser Ser Leu Val Leu Ala Ala His His Leu Pro Asp 150
727 Ala Val Phe Asp Asn Tyr Asp Arg Cys Gly Ala Ala Asn Glu Arg 165
728 Ala Arg Arg Leu Phe Arg Gly Ala Asp Glu Gly Leu Gly Ala Arg 180
729 Met Ala Phe His Thr Ala Asp Val Ala Thr Leu Thr Gly Glu Leu 195
730 Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala 210
731 Ala Glu Glu Lys Ala Gly Val Ile Ala His Leu Gly Ala His Met 225
732 Ala Asp Gly Ala Ala Leu Val Val Arg Thr Ala His Gly Ala Arg 240
733 Gly Phe Leu Tyr Pro Ile Val Asp Pro Glu Asp Val Arg Arg Gly 255
734 Gly Phe Asp Val Leu Ala Val Cys His Pro Glu Asp Glu Val Ile 270
735 Asn Ser Val Ile Val Ala Arg Lys Val Gly Ala Ala Ala Ala Ala 285
736 Ala Ala Ala Arg Arg Asp Glu Leu Ala Asp Ser Arg Gly Val Val 300
737 Leu Pro Val Val Gly Pro Pro Ser Thr Cys Cys Lys Val Glu Ala 315
738 Ser Ala Val Glu Lys Ala Glu Glu Phe Ala Ala Asn Lys Glu Leu 330

```

E--> 739 Ser Val *delete this*

345

741 <210> SEQ ID NO: 16
742 <211> LENGTH: 1372
743 <212> TYPE: DNA
744 <213> ORGANISM: Oryza sativa L.
746 <400> SEQUENCE: 16

```

E--> 750      10      20      30      40      50
E--> 751 ctccatttgg ttgtcatttt caactataat ccaccacaac tcgtgcaaca
E--> 752      60      70      80      90      100
E--> 753 tcagctcact cgtgttccca accgcgacaa agcttcacag atggaggctc
E--> 754      110     120     130     140     150
E--> 755 agaaccaaga ggctcgctgcc ctggctcgaga agatcgccgg cctccacgcc

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

E--> 756	160	170	180	190	200
E--> 757	gccatctcca	agctgccgtc	gctgagccca	tccgccgagg	tggacgcgct
E--> 758	210	220	230	240	250
E--> 759	cttcaccgac	ctcgtcacgg	cgtgcgtccc	ggcgagcccc	gtcgacgtgg
E--> 760	260	270	280	290	300
E--> 761	ccaagctcgg	cccggaggcg	caggcgatgc	gggaggagct	catccgcctc
E--> 762	310	320	330	340	350
E--> 763	tgtccgcgg	ccgagggcca	cctcgaggcg	cactacgccg	acatgctcgc
E--> 764	360	370	380	390	400
E--> 765	cgccttcgac	aaccgcgtcg	accacctcgc	ccgcttcccg	tactacggca
E--> 766	410	420	430	440	450
E--> 767	actacgtcaa	cctgagcaag	ctggagtacg	acctcctcgt	ccgctacgtc
E--> 768	460	470	480	490	500
E--> 769	cccggcattg	ccccaccgg	cgtcgccttc	gtcgggtcgg	gcccgcgtgc
E--> 770	510	520	530	540	550
E--> 771	gttcagctcc	ctcgtgctcg	ctgcgcacca	cctgccggac	gcggtgttcg
E--> 772	560	570	580	590	600
E--> 773	acaactacga	ccggtgcggc	gcggccaacg	agcgggcgag	gaggctgttc
E--> 774	610	620	630	640	650
E--> 775	cgcggcgccg	acgagggcct	cggcgcgcgc	atggcgttcc	acaccgccga
E--> 776	660	670	680	690	700
E--> 777	cgtggcgacc	ctgacggggg	agctcggcgc	gtacgacgtc	gtgttcctgg
E--> 778	710	720	730	740	750
E--> 779	cggcgctcgt	gggcatggcg	gccgaggaga	aggccggggt	gatcgcgcac
E--> 780	760	770	780	790	800
E--> 781	ctgggcgcgc	acatggcgga	cggcgcggcg	ctcgtcgtgc	ggacggcgca
E--> 782	810	820	830	840	850
E--> 783	cggggcgcgc	gggttcctgt	acccgatcgt	cgatcccgag	gacgtcaggc
E--> 784	860	870	880	890	900
E--> 785	gtggcggggtt	cgacgttctg	gcggtgtgcc	acccggagga	cgaggtgatc
E--> 786	910	920	930	940	950
E--> 787	aactccgtca	tcgtcgcccc	caaggctcgt	gccgcgcgcg	ccgcgcgcgc
E--> 788	960	970	980	990	1000
E--> 789	ggcgcgacga	gacgagctcg	cggactcgcg	cggcgtgggt	ctgccgggtg
E--> 790	1010	1020	1030	1040	1050
E--> 791	tcgggcccgc	gtccacgtgc	tgcaagggtg	aggcgagcgc	ggttgagaag
E--> 792	1060	1070	1080	1090	1100
E--> 793	gcagaagagt	ttgccgccaa	caaggagctg	tccgtctaac	agccggacga
E--> 794	1110	1120	1130	1140	1150
E--> 795	tcgaaaggcg	cactatatta	tggcaataaa	tcatttgatt	atacttatgc
E--> 796	1160	1170	1180	1190	1200
E--> 797	tgcatttgcg	aagctaaggt	atactatgca	agccatatgt	ttgtgttcgt
E--> 798	1210	1220	1230	1240	1250
E--> 799	acgtgttggt	tgggacgtac	agttgtgttg	ttgtacgtcg	tgaagtactg
E--> 800	1260	1270	1280	1290	1300
E--> 801	aagtgttcac	agtagatcac	aagttcacag	caatcaatga	ggaccctgta
E--> 802	1310	1320	1330	1340	1350
E--> 803	agccagtgtg	aacgaggaac	atgccatctg	tgtatgacag	tgagaaatta
E--> 804	1360	1370	1380		

Invalid

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

E--> 805 tataagaaaa acattttgtg ac
 808 <210> SEQ ID NO: 17
 809 <211> LENGTH: 320
 810 <212> TYPE: PRT
 811 <213> ORGANISM: Arabidopsis thaliana

W--> 812 <400> SEQUENCE: 17

814 Met Ala Cys Gln Asn Asn Leu Val Val Lys Gln Ile Ile Asp Leu	15
815 Tyr Asp Gln Ile Ser Lys Leu Lys Ser Leu Lys Pro Ser Lys Asn	30
816 Val Asp Thr Leu Phe Gly Gln Leu Val Ser Thr Cys Leu Pro Thr	45
817 Asp Thr Asn Ile Asp Val Thr Asn Met Cys Glu Glu Val Lys Asp	60
818 Met Arg Ala Asn Leu Ile Lys Leu Cys Gly Glu Ala Glu Gly Tyr	75
819 Leu Glu Gln His Phe Ser Thr Ile Leu Gly Ser Leu Gln Glu Asp	90
820 Gln Asn Pro Leu Asp His Leu His Ile Phe Pro Tyr Tyr Ser Asn	105
821 Tyr Leu Lys Leu Gly Lys Leu Glu Phe Asp Leu Leu Ser Gln His	120
822 Ser Ser His Val Pro Thr Lys Ile Ala Phe Val Gly Ser Gly Pro	135
823 Met Pro Leu Thr Ser Ile Val Leu Ala Lys Phe His Leu Pro Asn	150
824 Thr Thr Phe His Asn Phe Asp Ile Asp Ser His Ala Asn Thr Leu	165
825 Ala Ser Asn Leu Val Ser Arg Asp Pro Asp Leu Ser Lys Arg Met	180
826 Ile Phe His Thr Thr Asp Val Leu Asn Ala Thr Glu Ala Leu Asp	195
827 Gln Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Asp Lys	210
828 Glu Ser Lys Val Lys Ala Ile Glu His Leu Glu Lys His Met Ala	225
829 Pro Gly Ala Val Leu Met Leu Arg Arg Ala His Ala Leu Arg Ala	240
830 Phe Leu Tyr Pro Ile Val Asp Ser Ser Asp Leu Lys Gly Phe Gln	255
831 Leu Leu Thr Ile Tyr His Pro Thr Asp Asp Val Val Asn Ser Val	270
832 Val Ile Ala Arg Lys Leu Gly Gly Pro Thr Thr Pro Gly Val Asn	285
833 Gly Thr Arg Gly Cys Met Phe Met Pro Cys Asn Cys Ser Lys Ile	300
834 His Ala Ile Met Asn Asn Arg Gly Lys Lys Asn Met Ile Glu Glu	315
E--> 835 Phe Ser Thr Ile Glu	320
861 <210> SEQ ID NO: 19	
862 <211> LENGTH: 320	
863 <212> TYPE: PRT	
864 <213> ORGANISM: Arabidopsis thaliana	

W--> 865 <400> SEQUENCE: 19

867 Met Ala Cys Gln Asn Asn Leu Val Val Lys Gln Ile Met Asp Leu	15
868 Tyr Asn Gln Ile Ser Asn Leu Glu Ser Leu Lys Pro Ser Lys Asn	30
869 Val Asp Thr Leu Phe Arg Gln Leu Val Ser Thr Cys Leu Pro Thr	45
870 Asp Thr Asn Ile Asp Val Thr Glu Ile His Asp Glu Lys Val Lys	60
871 Asp Met Arg Ser His Leu Ile Lys Leu Cys Gly Glu Ala Glu Gly	75
872 Tyr Leu Glu Gln His Phe Ser Ala Ile Leu Gly Ser Phe Glu Asp	90
873 Asn Pro Leu Asn His Leu His Ile Phe Pro Tyr Tyr Asn Asn Tyr	105
874 Leu Lys Leu Gly Lys Leu Glu Phe Asp Leu Leu Ser Gln His Thr	120
875 Thr His Val Pro Thr Lys Val Ala Phe Ile Gly Ser Gly Pro Met	135
876 Pro Leu Thr Ser Ile Val Leu Ala Lys Phe His Leu Pro Asn Thr	150
877 Thr Phe His Asn Phe Asp Ile Asp Ser His Ala Asn Thr Leu Ala	165
878 Ser Asn Leu Val Ser Arg Asp Ser Asp Leu Ser Lys Arg Met Ile	180
879 Phe His Thr Thr Asp Val Leu Asn Ala Lys Glu Gly Leu Asp Gln	195
880 Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Asp Lys Glu	210
881 Ser Lys Val Lys Ala Ile Glu His Leu Glu Lys His Met Ala Pro	225
882 Gly Ala Val Val Met Leu Arg Ser Ala His Gly Leu Arg Ala Phe	240

*Invalid**Invalid*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:33

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

883 Leu Tyr Pro Ile Val Asp Ser Cys Asp Leu Lys Gly Phe Glu Val 255
 884 Leu Thr Ile Tyr His Pro Ser Asp Asp Val Val Asn Ser Val Val 270
 885 Ile Ala Arg Lys Leu Gly Gly Ser Asn Gly Ala Arg Gly Ser Gln 285
 886 Ile Gly Arg Cys Val Val Met Pro Cys Asn Cys Ser Lys Val His 300
 887 Ala Ile Leu Asn Asn Arg Gly Met Glu Lys Asn Leu Ile Glu Glu 315
 E--> 888 Phe Ser Ala Ile Glu 320
 915 <210> SEQ ID NO: 21
 916 <211> LENGTH: 320
 917 <212> TYPE: PRT
 918 <213> ORGANISM: Arabidopsis thaliana
 W--> 919 <400> SEQUENCE: 21
 921 Met Gly Cys Gln Asp Glu Gln Leu Val Gln Thr Ile Cys Asp Leu 15
 922 Tyr Glu Lys Ile Ser Lys Leu Glu Ser Leu Lys Pro Ser Glu Asp 30
 923 Val Asn Ile Leu Phe Lys Gln Leu Val Ser Thr Cys Ile Pro Pro 45
 924 Asn Pro Asn Ile Asp Val Thr Lys Met Cys Asp Arg Val Gln Glu 60
 925 Ile Arg Leu Asn Leu Ile Lys Ile Cys Gly Leu Ala Glu Gly His 75
 926 Leu Glu Asn His Phe Ser Ser Ile Leu Thr Ser Tyr Gln Asp Asn 90
 927 Pro Leu His His Leu Asn Ile Phe Pro Tyr Tyr Asn Asn Tyr Leu 105
 928 Lys Leu Gly Lys Leu Glu Phe Asp Leu Leu Glu Gln Asn Leu Asn 120
 929 Gly Phe Val Pro Lys Ser Val Ala Phe Ile Gly Ser Gly Pro Leu 135
 930 Pro Leu Thr Ser Ile Val Leu Ala Ser Phe His Leu Lys Asp Thr 150
 931 Ile Phe His Asn Phe Asp Ile Asp Pro Ser Ala Asn Ser Leu Ala 165
 932 Ser Leu Leu Val Ser Ser Asp Pro Asp Ile Ser Gln Arg Met Phe 180
 933 Phe His Thr Val Asp Ile Met Asp Val Thr Glu Ser Leu Lys Ser 195
 934 Phe Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Asn Lys Glu 210
 935 Glu Lys Val Lys Val Ile Glu His Leu Gln Lys His Met Ala Pro 225
 936 Gly Ala Val Leu Met Leu Arg Ser Ala His Gly Pro Arg Ala Phe 240
 937 Leu Tyr Pro Ile Val Glu Pro Cys Asp Leu Gln Gly Phe Glu Val 255
 938 Leu Ser Ile Tyr His Pro Thr Asp Asp Val Ile Asn Ser Val Val 270
 939 Ile Ser Lys Lys His Pro Val Val Ser Ile Gly Asn Val Gly Gly 285
 940 Pro Asn Ser Cys Leu Leu Lys Pro Cys Asn Cys Ser Lys Thr His 300
 941 Ala Lys Met Asn Lys Asn Met Met Ile Glu Glu Phe Gly Ala Arg 315
 E--> 942 Glu Glu Gln Leu Ser 320

Please see sample Sequence Listing
(attached) for valid format

FYI

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

<110> Smith, John; Smithgene Inc.
 <120> Example of a Sequence Listing
 <130> 01-00001
 <140> PCT/EP98/00001
 <141> 1998-12-31
 <150> US 08/999,999
 <151> 1997-10-15
 <160> 4
 <170> PatentIn version 2.0
 <210> 1
 <211> 389
 <212> DNA
 <213> Paramecium sp.
 <220>
 <221> CDS
 <222> (279)...(389)
 <300>
 <301> Doe, Richard
 <302> Isolation and Characterization of a Gene Encoding a
 Protease from Paramecium sp.
 <303> Journal of Genes
 <304> 1
 <305> 4
 <306> 1-7
 <307> 1988-06-31
 <308> 123456
 <309> 1988-06-31
 <400> 1
 agctgtagtc attcctgtgt cctcttctct ctgggcttct caccctgcta atcagatctc 60
 agggagagtg tcttgacctt cctctgcctt tgcagcttca caggcaggca ggcaggcagc 120
 tgatgtggca attgctggca gtgccacagg cttttcagcc aggcttaggg tgggttccgc 180
 cgcggcgcgg cggccctctt cgcgctcttc tcgcgcctct ctctcgtctt cctctcgtct 240

Appendix 3, page 2

[illegible]

[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M, when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO: #:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	O
<302>	Title		O
<303>	Journal		O
<304>	Volume		O
<305>	Issue		O
<306>	Pages		O
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	O
<308>	Database Accession Number	Accession number assigned by database including database name	O
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	O
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	O

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	0
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	0
<313>	Relevant Residues	FROM (position) TO (position)	0
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	0

5. Section 1.024 is revised to read as follows:

1.024 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.021(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:34

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:283 W: Missing Blank Line separator, <400> field identifier
L:39 M:252 E: No. of Seq. differs, <211>LENGTH:Input:328 Found:0 SEQ:1
L:46 M:283 W: Missing Blank Line separator, <400> field identifier
L:47 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:2
M:254 Repeated in SeqNo=2
L:48 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=2
L:118 M:283 W: Missing Blank Line separator, <400> field identifier
L:142 M:252 E: No. of Seq. differs, <211>LENGTH:Input:335 Found:0 SEQ:3
L:149 M:283 W: Missing Blank Line separator, <400> field identifier
L:151 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:4
M:254 Repeated in SeqNo=4
L:152 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=4
L:225 M:283 W: Missing Blank Line separator, <400> field identifier
L:249 M:252 E: No. of Seq. differs, <211>LENGTH:Input:335 Found:0 SEQ:5
L:256 M:283 W: Missing Blank Line separator, <400> field identifier
L:257 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:6
M:254 Repeated in SeqNo=6
L:258 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=6
L:328 M:283 W: Missing Blank Line separator, <400> field identifier
L:351 M:252 E: No. of Seq. differs, <211>LENGTH:Input:329 Found:0 SEQ:7
L:357 M:283 W: Missing Blank Line separator, <400> field identifier
L:359 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:8
M:254 Repeated in SeqNo=8
L:360 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=8
L:427 M:283 W: Missing Blank Line separator, <400> field identifier
L:447 M:252 E: No. of Seq. differs, <211>LENGTH:Input:282 Found:0 SEQ:9
L:453 M:283 W: Missing Blank Line separator, <400> field identifier
L:455 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:10
M:254 Repeated in SeqNo=10
L:456 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=10
L:513 M:283 W: Missing Blank Line separator, <400> field identifier
L:536 M:252 E: No. of Seq. differs, <211>LENGTH:Input:328 Found:0 SEQ:11
L:543 M:283 W: Missing Blank Line separator, <400> field identifier
L:545 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:0 SEQ:12
M:254 Repeated in SeqNo=12
L:546 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=12
L:619 M:283 W: Missing Blank Line separator, <400> field identifier
L:642 M:252 E: No. of Seq. differs, <211>LENGTH:Input:329 Found:0 SEQ:13
L:650 M:283 W: Missing Blank Line separator, <400> field identifier
L:652 M:254 E: No. of Bases conflict, LENGTH:Input:50 Counted:0 SEQ:14

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/674,337

DATE: 10/26/2001

TIME: 15:00:34

Input Set : A:\55107-sequence.txt

Output Set: N:\CRF3\10262001\I674337.raw

L:653 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
M:254 Repeated in SeqNo=14
L:653 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=14
L:715 M:283 W: Missing Blank Line separator, <400> field identifier
L:739 M:252 E: No. of Seq. differs, <211>LENGTH:Input:332 Found:0 SEQ:15
L:750 M:254 E: No. of Bases conflict, LENGTH:Input:50 Counted:0 SEQ:16
M:254 Repeated in SeqNo=16
L:751 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=16
L:812 M:283 W: Missing Blank Line separator, <400> field identifier
L:835 M:252 E: No. of Seq. differs, <211>LENGTH:Input:320 Found:0 SEQ:17
L:841 M:283 W: Missing Blank Line separator, <400> field identifier
L:843 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=18
L:865 M:283 W: Missing Blank Line separator, <400> field identifier
L:888 M:252 E: No. of Seq. differs, <211>LENGTH:Input:320 Found:0 SEQ:19
L:894 M:283 W: Missing Blank Line separator, <400> field identifier
L:897 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=20
L:919 M:283 W: Missing Blank Line separator, <400> field identifier
L:942 M:252 E: No. of Seq. differs, <211>LENGTH:Input:320 Found:0 SEQ:21
L:948 M:283 W: Missing Blank Line separator, <400> field identifier
L:950 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=22